

BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN OB-CADHERIN-1 POLYPEPTIDE SEQ ID NO: 16

Query: Cadherin-like plypeptide (SEQ ID NO: 4)
 Subjct: dbj|BAA04798.1| (D21254) OB-cadherin-1 [Homo sapiens] (SEQ ID NO: 16)
 Length = 796

Score = 1478 (525.3 bits), Expect = 2.1e-164, Sum P(2) = 2.1e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query:	283	GPALLRRRSWVNQFFVIEEYAGPEPVLIGKLHSDVDRGGRKYLTLTGEGAGTVFVID	462
		G L R++R WVNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID	
Sbjct:	45	GQVLQSRKRGWVNQFFVIEEYTGPDVPLVGRLHSDIDSGDGNIKYILSGEGAGTIFVID	104
Query:	463	EATGNIHVTKSLDREEKAQYVLLAQAVDRASNRPLEPPSEFIITKGQDINDNPPIFPLGPY	642
		+ +GNIH TK+LDREE+AQY L+AQAVDR +NRLEPPSEFI+K QDINDNPP F Y	
Sbjct:	105	DKSGNIHATKTLDREERAQYTLMAQAVDRDTRNPLEPPSEFIVKVDINDNPEEFLEHETY	164
Query:	643	HATPEMSNVGTSVIQVTAHDADDPYSGNSAKLVYTVTLVDGLPFFSVDPQTGVVVRTAIPNM	822
		HA VPE SNVGTSVIQVTA DADDP+YGNSAKLVY++L+G P+FSV+ QTG++RTA+PNM	
Sbjct:	165	HANVPERSNVGTSVIQVTAASDADDPYSGNSAKLVYSILEGQPYFSVEAQTGIIRTAIPNM	224
Query:	823	DRETQEEFLVVIQAKDMGGMGLSGSTTVTTLSDVNDNPPKFPQSLYQFSVVETAGPG	1002
		DRE +EE+ VVIQAKDMGGMGLSG+T VT+TL+DVNDNPPKFPQS+YQ SV E A PG	
Sbjct:	225	DREAKEYHVVIQAKDMGGMGLSGTTKVTITLTDVNDNPPKFPQSVYQISVSEAAVPG	284
Query:	1003	TLVGRLRAQDPDLGDNALMAYSILDCGSEAFSISTDLQGRDGLLTVRKPLDFESQRSYS	1182
		VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS	
Sbjct:	285	EEVGRVKAKDPDIGENGLVTYNIVDGDMGESFEITTDYETQEGVIKPKKPVDFETKRAYS	344
Query:	1183	FRVEATNTLIDPAYLRRGPFKDVASVRVAVQDAPEPAFTQAAAYHLTVPENKAPGTLVGQ	1362
		+VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+	
Sbjct:	345	LKVEAANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAAGTVVGR	404
Query:	1363	ISAADLSPASPIRYSILPHSDPERCFISIQPEEGTIHTAAPLDREARAWNHLTVLATEL	1539
		+ A D+ SPIRYSI H+D +R F+I PE+G I T PLDR E AW N+TV A E+	
Sbjct:	405	VHAKDPDAANSPIRYSIDRHTDLDRFFINPEDGFIKTKPLDREETAWNLNITVFAAEI	463

FIG. 1

**BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN
SEQUENCE ENCODED BY HUMAN OSF-4-1 CDNA POLYPEPTIDE SEQ ID NO: 17**

Query: Cadherin-like pypeptide (SEQ ID NO: 4)
 Subject: sp|R49731|R49731 Sequence encoded by human OSF-4-1 Cdna (SEQ ID NO: 17)
 Length = 796

Score = 1478 (525.3 bits), Expect = 1.2e-164, Sum P(2) = 1.2e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query: 283 GPALLRRSRWVNQFFVIEYAGPEPVLKLSHSDVDRGEGRTKYLLTGEAGTFFVID 462
 G L R++R WVNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID
 Sbjct: 45 GQVLQSKRGWVNQFFVIEEYTGPDPLVGLRLHSDIDS DGNIKYILSGEGAGTIFVID 104

Query: 463 EATGNIHVTKSLDREEKAQYVLLAQAVDRASNRPLEPPSEFIKQDINDNPPIFPLGPY 642
 + +GNIH TK+LDREE+AQY L+AQAVDR +NRPLEPPSEFI+K QDINDNPP F Y
 Sbjct: 105 DKSGNIHATKTLDREERAQYTLMAQAVDRDTRNPLEPPSEFIVKVDINDNPPFLHETY 164

Query: 643 HATVPEMSNVGTSVIQVTAHDADDPYGNLSAKLYVTVDGLPFFSFVDPPQTGVVRTAIPNM 822
 HA VPE SNVGTSVIQTVA DADDP+YGNLSAKLY++L+G P+FSV+ QTG++RTA+PNM
 Sbjct: 165 HANVPERSNVGTSVIQVTAHDADDPYGNLSAKLYVTVDGLPFFSFVDPPQTGVVRTAIPNM 224

Query: 823 DRETQEEFLVVIQAKDMGGMGGLSGSTTVTTLSDVNDNPPKFPQSLYQFSVVETAGPG 1002
 DRE +EE+ VVIQAKDMGGMGGLSG+T VT+TL+DVNDNPPKFPQS+YQ SV E A PG
 Sbjct: 225 DREAEEYHVVIQAKDMGGMGGLSGTKVTITLTDVNDNPPKFPQSVYQISVSEAAVPG 284

Query: 1003 TLVGRRLRAQDPDLGDNALMAYSILDEGESEAFSISTDLQGRDGLLTVRKPLDFESQRSYS 1182
 VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS
 Sbjct: 285 EEVGRVKAKDPDIGENGLVTYNIVDGDMESFEITTDYETQEGVIKPKPVDFTKRAYS 344

Query: 1183 FRVEATNTLIDPAYLRGPFKDVASVRVAVQDAPEPAFTQAAAYHLLTVPENKAPGTLVGQ 1362
 +VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+
 Sbjct: 345 LKVEAANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAAGTVVGR 404

Query: 1363 ISAADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARAWHNLTVIATEL 1539
 + A D+ SPIRYSI H+D +R F+I PE+G I T PLDRE AW N+TV A E+
 Sbjct: 405 VHAKDPDAANSPIRYSIDRHTDLDRFTINPEDGFIKTKPLDREATAWLNITVFAAEI 463

FIG. 2